



#12

SEQUENCE LISTING

<110> Prussak, Charles E
Kipps, Thomas J
Cantwell, Mark J

<120> Novel Chimeric TNF Ligands

<130> UCSD 263/092

<140> US 10/006,305

<141> 2001-12-06

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric DNA construct comprising Domain IV of hTNFa linked to
Domains I, II, and III of hCD154

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ttactgaact	gtgaggagat	taaaagccag	tttgaaggct	ttgtgaagga	tataatgtta	300
aacaaagagg	agacgaagaa	agatgaggat	cctgtagccc	atgttgtagc	aaaccctcaa	360
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gagctgagag	ataaccagct	ggtgggtgcca	tcagagggcc	tgtacctcat	ctactcccag	480
gtcctcttca	agggccaaag	ctgcccttcc	acccatgtgc	tcctcaccca	caccatcagc	540
cgcacgcgcg	tctcttacca	gaccaaggtc	aacctctctc	ctgccatcaa	gagcccctgc	600
cagagggaga	ccccagaggg	ggctgaggcc	aagccctggt	atgagcccat	ctatctggga	660
ggggtcttcc	agctggagaa	gggtgaccga	ctcagcgctg	agatcaatcg	gcccgactat	720
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<210> 2

<211> 580

<212> DNA

<213> Artificial Sequence

<220>

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ttcgcacagg	ctgcggatcc	tgtagcccat	gttgtagcaa	accctcaagc	tgaggggcag	180
ctccagtggc	tgaaccgccg	ggccaatgcc	ctcctggcca	atggcgtgga	gctgagagat	240
aaccagctgg	tggtgccatc	agagggcctg	tacctcatct	actcccaggt	cctcttcaag	300
ggccaaggct	gcccctccac	ccatgtgctc	ctcaccacaca	ccatcagccg	catcgccgtc	360
tcctaccaga	ccaaggtcaa	cctcctctct	gccatcaaga	gcccttgcca	gagggagacc	420
ccagaggggg	ctgaggccaa	gccctgggtat	gagcccatct	atctgggagg	ggtcttccag	480
ctggagaagg	gtgaccgact	cagcgctgag	atcaatcggc	cgcactatct	cgactttgcg	540
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<210> 3

<211> 837

<212> DNA

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<223> Chimeric DNA construct comprising Domain IV of hTNFa linked to Domains I, II, and III of hFasL

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ggcgtggagc	tgagagataa	ccagctgggtg	gtgccatcag	agggcctgta	cctcatctac	540
tccaggtcc	tcttcaaggg	ccaaggctgc	ccctccaccc	atgtgctcct	caccacacc	600
atcagccgca	tcgccgtctc	ctaccagacc	aaggtcaacc	tcctctctgc	catcaagagc	660
ccctgccaga	gggagacccc	agagggggct	gaggccaagc	cctgggtatga	gcccatctat	720
ctgggagggg	tcttccagct	ggagaagggt	gaccgactca	gcgctgagat	caatcgcccc	780
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<210> 4

<211> 813

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric DNA construct comprising Domain IV of hTNFa linked to

Domains I, II, and III of hTRAIL

<400> 4

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gagctgaagc agatgcagga caagtactcc aaaagtggca ttgcttgttt cttaaagaa      180
gatgacagtt attgggaccc caatgacgaa gagagtatga acagcccctg ctggcaagtc      240
aagtggcaac tccgtcagct cgtagaaag atgattttga gaacctctga ggaaaccatt      300
tctacagttc aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtcctcag      360
agagtagcgg atcctgtagc ccatgttgta gcaaaccctc aagctgaggg gcagctccag      420
tggtgaacc gccgggcaa tgccctcctg gccaatggcg tggagctgag agataaccag      480
ctggtggtgc catcagaggg cctgtacctc atctactccc aggtcctctt caagggccaa      540
ggctgcccct ccacccatgt gctcctcacc cacaccatca gccgcatcgc cgtctcctac      600
cagaccaagg tcaacctcct ctctgccatc aagagcccct gccagagggg gacccagag      660
ggggctgagg ccaagccctg gtatgagccc atctatctgg gaggggtctt ccagctggag      720
aagggtgacc gactcagcgc tgagatcaat cggcccgaact atctcgactt tgcggagtct      780
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<210> 5

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<212> PRT

<213> Artificial Sequence

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<400> 5

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          20           25           30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
          35           40           45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
          50           55           60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65           70           75           80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
          85           90           95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Asp Glu Asp Pro Val

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100						105						110					
Ala	His	Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu		
115						120						125					
Asn	Arg	Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp		
130						135						140					
Asn	Gln	Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln		
145						150						155					
Val	Leu	Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr		
165						170						175					
His	Thr	Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu		
180						185						190					
Leu	Ser	Ala	Ile	Lys	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala		
195						200						205					
Glu	Ala	Lys	Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln		
210						215						220					
Leu	Glu	Lys	Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr		
225						230						235					
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NO.: 2																	
<400> 6																	
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Cys	Val	Leu	Arg	Ala	Ala	Leu	Val	Pro	Leu	Val	Ala	Gly	Leu	Val	Ile		
20						25						30					
Cys	Leu	Val	Val	Cys	Ile	Gln	Arg	Phe	Ala	Gln	Ala	Ala	Asp	Pro	Val		
35						40						45					

Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu
 50 55 60

Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
 65 70 75 80

Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
 85 90 95

Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr
 100 105 110

His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu
 115 120 125

Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala
 130 135 140

Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln
 145 150 155 160

Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr
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Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
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<210> 7

<211> 278

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric TNFa polypeptide encoded by the DNA sequence of SEQ ID
 NO.: 3

<400> 7

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Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys
 20 25 30

Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro
 35 40 45

Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro
 50 55 60

Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly
 65 70 75 80

Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly
 85 90 95

Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala
 100 105 110

Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu
 115 120 125

Lys Gln Ala Asp Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
 130 135 140

Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
 145 150 155 160

Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu
 165 170 175

Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
 180 185 190

Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
 195 200 205

Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
 210 215 220

Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
 225 230 235 240

Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
 245 250 255

Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
 260 265 270

Phe Gly Ile Ile Ala Leu
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<210> 8

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric TNFa polypeptide encoded by the DNA sequence of SEQ ID NO.: 4

<400> 8

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Val	Leu	Ile	Val	Ile	Phe	Thr	Val	Leu	Leu	Gln	Ser	Leu	Cys	Val	Ala
			20					25					30		

Val	Thr	Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	Gln	Met	Gln	Asp	Lys
		35					40					45			

Tyr	Ser	Lys	Ser	Gly	Ile	Ala	Cys	Phe	Leu	Lys	Glu	Asp	Asp	Ser	Tyr
	50					55					60				

Trp	Asp	Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	Pro	Cys	Trp	Gln	Val
65					70				75					80	

Lys	Trp	Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Met	Ile	Leu	Arg	Thr	Ser
			85						90					95	

Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro
			100					105					110		

Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Asp	Pro	Val	Ala	His
		115					120					125			

Val	Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg
		130				135						140			

Arg	Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln
145					150					155					160

Leu	Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu
				165					170					175	

Phe	Lys	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr
			180					185					190		

Ile	Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser
		195					200					205			

Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
210 215 220

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
225 230 235 240

Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
245 250 255

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
260 265 270